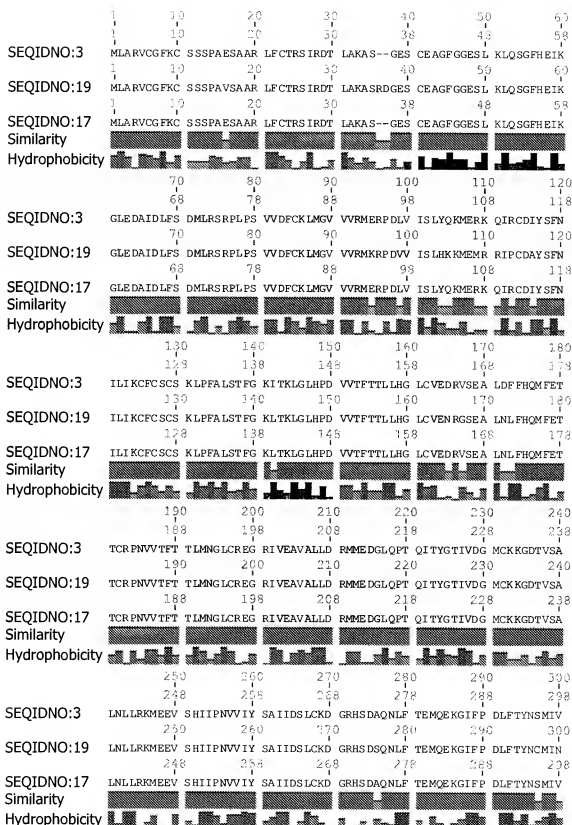
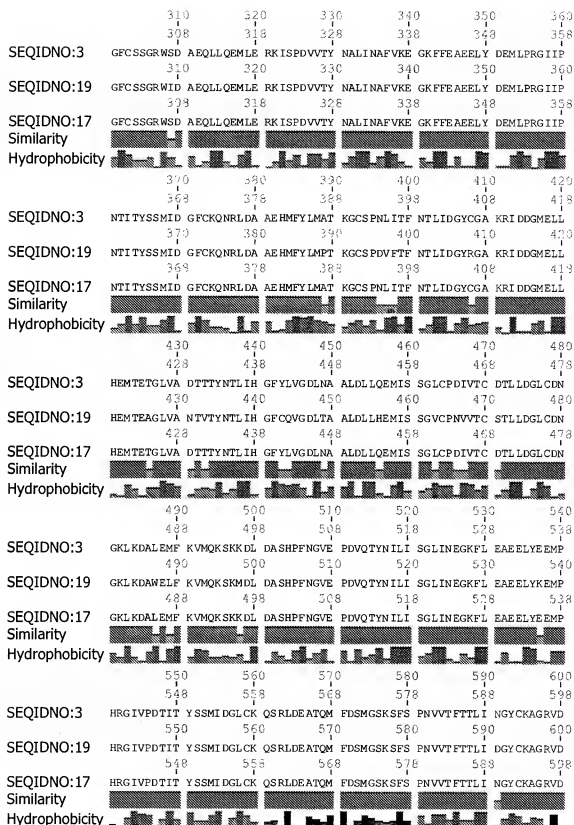
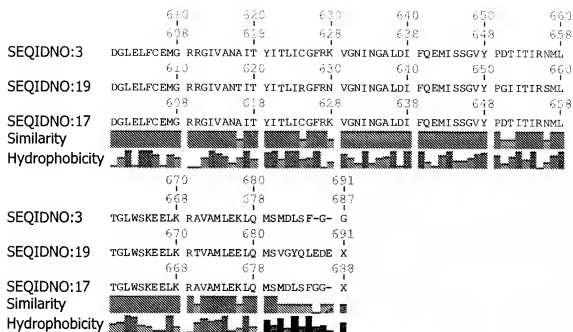


Application No.	: 10/613,053	Confirmation No.:	6718
Applicant:	: Imamura		
Filed:	: July 7, 2003		
Group Art Unit:	1638		
Examiner:	: FOX, David T.		
For	: Protein Involved in Restoration of Cytoplasmic Male Sterility to Fertility and Gene Encoding the Protein and Gene		
Docket No.	: 54-05A		
Customer No.	: 23713		

APPENDIX A and APPENDIX B







	1	10	20	30	40	50	60	70
seqidno2	1	10	20	30	40	50	60	70
	1	10	20	30	40	50	60	70
seqidno18	1	10	20	30	40	50	60	70
seqidno16	1	10	20	30	40	50	60	70
Similarity								
	80	90	100	110	120	130	140	
seqidno2	80	90	100	106	114	124	134	
	80	90	100	110	120	130	140	
seqidno18	80	90	100	106	114	124	134	
seqidno16	80	90	100	106	114	124	134	
Similarity								
	150	160	170	180	190	200	210	
seqidno2	144	154	164	174	184	194	204	
	150	160	170	180	190	200	210	
seqidno18	144	154	164	174	184	194	204	
seqidno16	144	154	164	174	184	194	204	
Similarity								
	220	230	240	250	260	270	280	
seqidno2	214	224	234	244	254	264	274	
	220	230	240	250	260	270	280	
seqidno18	214	224	234	244	254	264	274	
seqidno16	214	224	234	244	254	264	274	
Similarity								
	290	300	310	320	330	340	350	
seqidno2	284	294	304	314	321	331	341	
	290	300	310	320	330	340	350	
seqidno18	284	294	304	314	321	331	341	
seqidno16	284	294	304	314	321	331	341	
Similarity								

	360	370	380	390	400	410	420
seqidno2	ATACAGCTTC	AATATTCTGA	TAAAAATGTT	CTGCAGCTGC	TCTAAGCTCC	CCTTTGCTTT	GTCTACATTT
seqidno18	ATACAGCTTC	AATATTCTGA	TAAAGTGTT	CTGCAGCTGC	TCTAAGCTGC	CCTTTGCTTT	GTCTACATTT
seqidno16	ATACAGCTTC	AATATTCTGA	TAAAAATGTT	CTGCAGCTGC	TCTAAGCTCC	CCTTTGCTTT	GTCTACATTT
Similarity							
	430	440	450	460	470	480	490
seqidno2	GGTAAGATCA	CCAAGCTTGG	ACTCCACCTC	GATGTTGTTA	CCTTCACCAC	CCTGCTCCAT	GGATTATGTG
seqidno18	GGTAAGATCA	CCAAGCTTGG	ACTCCACCTC	GATGTTGTTA	CCTTCACCAC	CCTTCTCCAC	GGATTGTGTG
seqidno16	GGTAAGCTCA	CCAAGCTTGG	ACTCCACCTC	GATGTTGTTA	CCTTCACCAC	CCTGCTCCAC	GGATTGTGGG
Similarity							
	500	510	520	530	540	550	560
seqidno2	TGGAAGATAG	GGTTTCTGAA	GCCTTGGATT	TTTTCATCA	AATGTTTGAA	ACGACATGTA	GGCCCAATGT
seqidno18	TGGAATAATG	GGGTTCTGAA	GCTTTGAATT	TGTTTCATCA	AATGTTTGAA	ACGRCATGTA	GGCCCAATGT
seqidno16	TGGAAGATAG	GGTTTCTGAA	GCCTTGAATT	TTTTCATCA	AATGTTTGAA	ACGACATGTA	GGCCCAATGT
Similarity							
	570	580	590	600	610	620	630
seqidno2	CGTAACCTTC	ACCACCTTGA	TGAACGGTCT	TTGCGCGGAG	GGTAGAATTG	TGGAAGCCGT	AGCTCTGCTT
seqidno18	CGTAACCTTC	ACCACCTTGA	TGAACGGTCT	TTGCGCGGAG	GGTAGAATTG	TGGAAGCCGT	AGCTCTACTT
seqidno16	CGTAACCTTC	ACCACCTTGA	TGAACGGTCT	TTGCGCGGAG	GGTAGAATTG	TGGAAGCCGT	AGCTCTGCTT
Similarity							
	640	650	660	670	680	690	700
seqidno2	GATCGGATGA	TGGAAATGTT	TCTCCAGCCT	ACCCAGATTG	CTTATGGAAC	AATCGTAGAT	GGGATGTGTA
seqidno18	GATCGGATGA	TGGAAATGTT	TCTCCAGCCT	ACCCAGATTG	CTTATGGAAC	AATCGTAGAT	GGGATGTGTA
seqidno16	GATCGGATGA	TGGAAATGTT	TCTCCAGCCT	ACCCAGATTG	CTTATGGAAC	AATCGTAGAT	GGGATGTGTA
Similarity							

	710	720	730	740	750	760	770
	701	711	721	731	741	751	761
seqidno2	AGAAGGGAGA	TACTGTGTCT	GCACCTGAATC	TGCTGAGGAA	GATGGAGGAG	GTGAGCCACA	TCATACCCAA
	707	717	727	737	747	757	767

seqidno18	AGAAGGGAGA	TACTGTGTCT	GCACCTGAATC	TGCTGAGGAA	GATGGAGGAG	GTGAGCCACA	TCATACCCAA
	701	711	721	731	741	751	761

seqidno16	AGAAGGGAGA	TACTGTGTCT	GCACCTGAATC	TGCTGAGGAA	GATGGAGGAG	GTGAGCCACA	TCATACCCAA
Similarity							

	780	790	800	810	820	830	840
	771	781	791	801	811	821	831
seqidno2	TGTTGTAATC	TATAGTGCAA	TCATTGATAG	CCTTTGTAAA	GACGGACGTC	ATAGCGATGC	ACAAATCTT
	777	787	797	807	817	827	837

seqidno18	TGTTGTAATC	TATAGTGCAA	TCATTGATAG	CCTTTGTAAA	GACGGACGTC	ATAGCGATTC	TCAAATCTT
	771	781	791	801	811	821	831

seqidno16	TGTTGTAATC	TATAGTGCAA	TCATTGATAG	CCTTTGTAAA	GACGGACGTC	ATAGCGATGC	ACAAATCTT
Similarity							

	850	860	870	880	890	900	910
	841	851	861	871	881	891	901
seqidno2	TTCACGAAA	TGCAAGAGAA	AGGAATCTTT	CCCGATTAT	TTACCTACAA	CAGTATGAT	AGTTGGTTT
	847	857	867	877	887	897	907

seqidno18	TTCACGAAA	TGCAAGAGAA	AGGAATCTTT	CCCGATTAT	TTACCTACAA	CTGTATGATC	AA--CGGGTT
	841	851	861	871	881	891	899

seqidno16	TTCACGAAA	TGCAAGAGAA	AGGAATCTTT	CCCGATTAT	TTACCTACAA	CAGTATGAT	AGTTGGTTT
Similarity							

	920	930	940	950	960	970	980
	909	919	929	939	949	959	969
seqidno2	TTGTAGCTCT	GGTAGATGGA	GCGACGCGGA	GCAGTTGTTG	CAAGAAATGT	TAGAAAGGAA	GATCAGCCCT
	915	925	935	945	955	965	975

seqidno18	TTGTAGCTCT	GGTAGATGGA	TCGACGCGGA	GCAGTTGTTG	CAAGAAATGT	TAGAAAGGAA	GATCAGCCCT
	909	919	929	939	949	959	969






seqidno16	TTGTAGCTCT	GGTAGATGGA	GCGACGCGGA	GCAGTTGTTG	CAAGAAATGT	TAGAAAGGAA	GATCAGCCCT
Similarity							

	990	1,000	1,010	1,020	1,030	1,040	1,050
	979	989	999	1,009	1,019	1,029	1,039
seqidno2	GATGTTGTAA	CTTATAATGC	TTTGATCAAT	GCATTTGTCA	AGGAAGGCAA	GTTCTTTGAG	GCTGAAGAAT
	985	995	1,005	1,015	1,025	1,035	1,045

seqidno18	GATGTTGTAA	CTTATAATGC	TTTGATCAAT	GCATTTGTCA	AGGAAGGCAA	GTTCTTTGAG	GCTGAAGAAT
	979	989	999	1,009	1,019	1,029	1,039

seqidno16	GATGTTGTAA	CTTATAATGC	TTTGATCAAT	GCATTTGTCA	AGGAAGGCAA	GTTCTTTGAG	GCTGAAGAAT
Similarity							

		1,060	1,070	1,080	1,090	1,100	1,110	1,120
		1,049	1,059	1,069	1,079	1,089	1,099	1,109
seqidno2	TATACGATGA	GATGCTTCCA	AGGGGTATAA	TCCTAAATAC	AATCACATAT	AGTTCAATGA	TCGATGGATT	
		1,055	1,065	1,075	1,085	1,095	1,105	1,115
seqidno18	TATACGATGA	GATGCTTCTT	AGGGGTATAA	TCCTAAATAC	AATCACATAT	AGTTCAATGA	TCGATGGATT	
		1,045	1,059	1,069	1,079	1,089	1,099	1,109
seqidno16	TATACGATGA	GATGCTTCCA	AGGGGTATAA	TCCTAAATAC	AATCACATAT	AGTTCAATGA	TCGATGGATT	
Similarity								
		1,130	1,140	1,150	1,160	1,170	1,180	1,190
		1,119	1,129	1,139	1,149	1,159	1,169	1,179
seqidno2	TTGCAACAG	AATCGTCTTG	ATGCTGCTGA	GCACATGTTT	TATTTGATGG	CTACCAAGGG	CTGCTCTCCC	
		1,125	1,135	1,145	1,155	1,165	1,175	1,185
seqidno18	TTGCAACAG	AATCGTCTTG	ATGCTGCTGA	GCACATGTTT	TATTTGATGC	CTACCAAGGG	CTGCTCTCCG	
		1,119	1,129	1,139	1,149	1,159	1,169	1,179
seqidno16	TTGCAACAG	AATCGTCTTG	ATGCTGCTGA	GCACATGTTT	TATTTGATGG	CTACCAAGGG	CTGCTCTCCC	
Similarity								
		1,200	1,210	1,220	1,230	1,240	1,250	1,260
		1,189	1,199	1,209	1,219	1,229	1,239	1,249
seqidno2	AACCTAATCA	CTTTCAATAC	TCTCATAGAC	GGATATTGTG	GGGCTAAGAG	GATAGATGAT	GGAATGGAAC	
		1,195	1,205	1,215	1,225	1,235	1,245	1,255
seqidno18	GACGTATTCA	CTTTCAATAC	TCTCATAGAC	GGATATCTGT	GGGCTAAGAG	GATAGATGAT	GGAATGGAAC	
		1,189	1,199	1,209	1,219	1,229	1,239	1,249
seqidno16	AACCTAATCA	CTTTCAATAC	TCTCATAGAC	GGATATTGTG	GGGCTAAGAG	GATAGATGAT	GGAATGGAAC	
Similarity								
		1,270	1,280	1,290	1,300	1,310	1,320	1,330
		1,259	1,269	1,279	1,289	1,299	1,309	1,319
seqidno2	TTCTCCATGA	GATGACTGAA	ACAGGATTAG	TTGCTGACAC	AACACTCTTAC	AACACTCTTA	TTCACGGGTT	
		1,265	1,275	1,285	1,295	1,305	1,315	1,325
seqidno18	TTCTCCATGA	GATGACTGAA	GCAGGATTAG	TTGCTAACAC	AGTTACTTAC	AACACTCTTA	TTCACGGGTT	
		1,269	1,269	1,279	1,289	1,299	1,309	1,319
seqidno16	TTCTCCATGA	GATGACTGAA	ACAGGATTAG	TTGCTGACAC	AACACTCTTAC	AACACTCTTA	TTCACGGGTT	
Similarity								
		1,340	1,350	1,360	1,370	1,380	1,390	1,400
		1,329	1,339	1,349	1,359	1,369	1,379	1,389
seqidno2	CTATCTGGTG	GGCGACTCTTA	ATGCTGCTCT	AGACCTTTTA	CAAGAGATGA	TCTCTAGTGG	TTTGTGCCCT	
		1,335	1,345	1,355	1,365	1,375	1,385	1,395
seqidno18	TTGTCAGGTG	GGCGACTCTTA	CTGCTGCTCT	AGACCTTCTA	CATGAGATGA	TTTCTAGTGG	TGTGTGCCCT	
		1,329	1,339	1,349	1,359	1,369	1,379	1,389
seqidno16	CTATCTGGTG	GGCGACTCTTA	ATGCTGCTCT	AGACCTTTTA	CAAGAGATGA	TCTCTAGTGG	TTTGTGCCCT	
Similarity								

	1,410	1,420	1,430	1,440	1,450	1,460	1,470
	1,399	1,409	1,419	1,429	1,439	1,449	1,459
seqidno2	GATATCGTTA CTTGTGACAC TTTGCTGGAT GGCTCTCGG ATAATGGGAA ACTAAAAGAT GCATTGGAAA						
	1,405	1,415	1,425	1,435	1,445	1,455	1,465
seqidno18	AATGTCGTTA CTTGTAGCAC TTTGCTGGAT GGCTCTCGG ATACGGGAA ACTAAAAGAT GCATGGGAA						
	1,399	1,409	1,419	1,429	1,439	1,449	1,459
seqidno16	GATATCGTTA CTTGTGACAC TTTGCTGGAT GGCTCTCGG ATAATGGGAA ACTAAAAGAT GCATTGGAAA						
Similarity							
	1,480	1,490	1,500	1,510	1,520	1,530	1,540
	1,469	1,479	1,489	1,499	1,509	1,519	1,529
seqidno2	TGTTTAAAGT TATGCAGAAG AGTAAGAAGG ATCTTGATGC TAGTCACCCC TTCATGGTG TGGAACTGA						
	1,475	1,485	1,495	1,505	1,515	1,525	1,535
seqidno18	TGTTTAAAGT TATGCAGAAG AGTAAGAAGG ATCTTGATGC TAGTCACCCC TTCATGGTG TGGAACTGA						
	1,469	1,479	1,489	1,499	1,509	1,519	1,529
seqidno16	TGTTTAAAGT TATGCAGAAG AGTAAGAAGG ATCTTGATGC TAGTCACCCC TTCATGGTG TGGAACTGA						
Similarity							
	1,550	1,560	1,570	1,580	1,590	1,600	1,610
	1,539	1,549	1,559	1,569	1,579	1,589	1,599
seqidno2	TGTTCAAAC TACAAATAT TGATCAGCGG CTGTGATCAAT GAAGGGAAGT TTTTAGAGGC CGAGGAATTA						
	1,545	1,555	1,565	1,575	1,585	1,595	1,605
seqidno18	TGTTCAAAC TACAAATAT TGATCAGCGG CTGTGATCAAT GAAGGGAAGT TTTTAGAGGC CGAGGAATTA						
	1,539	1,549	1,559	1,569	1,579	1,585	1,599
seqidno16	TGTTCAAAC TACAAATAT TGATCAGCGG CTGTGATCAAT GAAGGGAAGT TTTTAGAGGC CGAGGAATTA						
Similarity							
	1,620	1,630	1,640	1,650	1,660	1,670	1,680
	1,609	1,619	1,629	1,639	1,649	1,659	1,669
seqidno2	TACGAGGAGA TGCCCCACAG GGGTATAGTC CCAGATACTA TCACCTATAG CTCATGATC GATGGATTAT						
	1,615	1,625	1,635	1,645	1,655	1,665	1,675
seqidno18	TACAAGGAGA TGCCCCACAG GGGTATAGTC CCAGATACTA TTACCTATAG CTCATGATC GATGGACTAT						
	1,609	1,619	1,629	1,639	1,649	1,659	1,669
seqidno16	TACGAGGAGA TGCCCCACAG GGGTATAGTC CCAGATACTA TCACCTATAG CTCATGATC GATGGATTAT						
Similarity							
	1,690	1,700	1,710	1,720	1,730	1,740	1,750
	1,679	1,689	1,699	1,709	1,719	1,729	1,739
seqidno2	GCAAGCAGAG CCGCTAGAT GAGGCTACAC AAATGTTGA TTCGATGGGT AGCAAGAGCT TCTCTCCAAA						
	1,685	1,695	1,705	1,715	1,725	1,735	1,745
seqidno18	GCAAGCAGAG CCGCTAGAT GAGGCTACAC AAATGTTGA TTCGATGGGT AGCAAGAGCT TCTCTCCAAA						
	1,679	1,689	1,699	1,709	1,719	1,729	1,739
seqidno16	GCAAGCAGAG CCGCTAGAT GAGGCTACAC AAATGTTGA TTCGATGGGT AGCAAGAGCT TCTCTCCAAA						
Similarity							

	1,760	1,770	1,780	1,790	1,800	1,810	1,820
	1,749	1,759	1,769	1,779	1,789	1,799	1,809
seqidno2	CGTAGTGACC	TTTACTACAC	TCATTAATGG	CTACTGTAAG	GCAGGAAGGG	TTGATGATGG	GCTGGAGCTT
	1,755	1,765	1,775	1,785	1,795	1,805	1,815
seqidno18	CGTAGTGACC	TTTACTACAC	TCATTTGATGG	CTACTGTAAA	GCAGGAAGGG	TTGATGATGG	GCTGGAGCTT
	1,749	1,759	1,769	1,779	1,789	1,799	1,809
seqidno16	CGTAGTGACC	TTTACTACAC	TCATTAATGG	CTACTGTAAG	GCAGGAAGGG	TTGATGATGG	GCTGGAGCTT
Similarity							
	1,830	1,840	1,850	1,860	1,870	1,880	1,890
	1,819	1,829	1,839	1,849	1,859	1,869	1,879
seqidno2	TTCTGCGAGA	TGGGTGAAG	AGGGATAGTT	GCTAACGCAA	TTACTTACAT	CACITTTGATT	TGTGTTTTTC
	1,825	1,835	1,845	1,855	1,865	1,875	1,885
seqidno18	TTCTGCGAGA	TGGGTAGAAG	AGGGATAGTT	GCTAATACAA	TTACTTACAT	CACITTTGATT	CGTGTTTTTC
	1,819	1,829	1,839	1,849	1,859	1,869	1,879
seqidno16	TTCTGCGAGA	TGGGTGAAG	AGGGATAGTT	GCTAACGCAA	TTACTTACAT	CACITTTGATT	TGTGTTTTTC
Similarity							
	1,900	1,910	1,920	1,930	1,940	1,950	1,960
	1,889	1,899	1,909	1,919	1,929	1,939	1,949
seqidno2	GTAAGTGGG	TAATATTAAT	GGGGCTCTAG	ACATTTTCCA	GGAGATGATT	TCAAGTGGTG	TGTATCCTGA
	1,895	1,905	1,915	1,925	1,935	1,945	1,955
seqidno18	GCAATGTGGG	TAATATTAAT	GGGGCTCTAG	ACATTTTCCA	GGAGATGATT	TCAAGTGGTG	TGTATCCTGG
	1,889	1,899	1,909	1,919	1,929	1,939	1,949
seqidno16	GTAAGTGGG	TAATATTAAT	GGGGCTCTAG	ACATTTTCCA	GGAGATGATT	TCAAGTGGTG	TGTATCCTGA
Similarity							
	1,970	1,980	1,990	2,000	2,010	2,020	2,030
	1,959	1,969	1,979	1,989	1,999	2,009	2,019
seqidno2	TACCATTACC	ATCCGCAATA	TGCTGACTGG	TTTATGGAGT	AAAGAGGAAC	TAAAAGGGC	AGTGCAATG
	1,965	1,975	1,985	1,995	2,005	2,015	2,025
seqidno18	TATCATTACT	ATCCGAGTA	TGCTGACTGG	TTTATGGAGT	AAAGAGGAAC	TAAAAGGAC	AGTGCAATG
	1,959	1,969	1,979	1,989	1,999	2,009	2,019
seqidno16	TACCATTACC	ATCCGCAATA	TGCTGACTGG	TTTATGGAGT	AAAGAGGAAC	TAAAAGGGC	AGTGCAATG
Similarity							
	2,040	2,050	2,060	2,070	2,079		
	2,029	2,039	2,049	2,064			
seqidno2	CTTGAGAAAC	TGCAGATGAG	TATGGATCTA	TCATTGSGGG	GATGA----		
	2,035	2,045	2,054	2,064	2,073		
seqidno18	CTTGAGGAACT	TGCAGATGAG	TGTGGGG-TA	TCAGTTGGAG	GATGAATGA		
	2,029	2,039	2,049	2,064			
seqidno16	CTTGAGAAAC	TGCAGATGAG	TATGGATCTA	TCATTGSGGG	GATGA----		
Similarity							